

**AMENDMENT TO THE SPECIFICATION**

Please amend the specification as follows:

Please replace the paragraph spanning pages 27 to 28, with the following amended paragraph (which is also paragraph [0123] of the corresponding publication, U.S. Pat. App. Pub. No. 20030049815):

**[0123]** The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are preferably identified (i.e., aligned) by means of a scoring matrix, many of which are known in the art. Preferably, the scoring matrix used is the BLOSUM62 matrix (Gonnet et al., Science 256:1443-1445, 1992; Henikoff and Henikoff, Proteins 17:49-61, 1993). Less preferably, the PAM or PAM250 matrices may also be used (see, e.g., Schwartz and Dayhoff, eds., 1978, Matrices for Detecting Distance Relationships: Atlas of protein Sequence and Structure, Washington: National Biomedical Research Foundation). BLAST programs are accessible through the U.S. National Library of Medicine, ~~e.g., at~~ [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov).